

Abstract of the Disclosure

The method of displaying sequences of the present invention adds visual characteristics in accordance with the mutations and/or similarities in a plurality of similar nucleotide sequences or amino acid sequences. These visual characteristics are added to regions of mutation and/or regions of similarity, and further, are added in accordance with the degree of mutation and/or similarity and in accordance with the frequency of mutation in the regions of mutation. In addition, nucleotide sequences are converted to amino acid sequences, and the visual characteristics are added based on amino acid information that includes the names or properties of amino acids that correspond to codons of the regions of mutation. Links are provided to information that relates to a plurality of similar nucleotide sequences or amino acid sequences. The homology search method of the present invention uses this sequence display method to display search results.